

SEQUENCE LISTING

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<120> Biological Products

<130> Carp-0089

<140> 09/875,221

<141> 2001-06-06

<150> GB0013810.7

<151> 2000-06-06

<160> 130

<170> PatentIn version 3.1

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gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac 96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
35 40 45

tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
50 55 60

tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

aca ttc ggt cag ggt act aaa gta gaa atc aaa 321
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20 25 30

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35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30
 gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa ctc ctc atc 144
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
 50 55 60
 tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
 85 90 95
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 35 40 45
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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tcc gtc aaa gtt tgc tgt aag gcc tca ggc tac gtg ttc aca gac tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30
ggt atg aat tgg gtc aga cag gcc ccg gga caa ggc ctg gaa tgg atg 144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
ggt tgg att aat act tac att gga gag cct att tat gct caa aag ttc 192
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
50 55 60
cag ggc aga gtc acg ttc act cta gac acc tcc aca agc act gca tac 240
Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
atg gag ctg tca tct ctg aga tcc gag gac acc gca gtg tac tat tgt 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc 336
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
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Leu Val Thr Val Ser Ser
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr
 20 25 30
 gga atg aat tgg gtt aga cag gcc ccg gga aag ggc ctg gaa tgg atg 144
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 ggt tgg att aat act tac att gga gag cct att tat gct gac agc gtc 192
 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
 50 55 60
 aag ggc aga ttc acg ttc tct cta gac aca tcc aag tca aca gca tac 240
 Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
 65 70 75 80
 ctc caa atg aat agc ctg aga gca gag gac acc gca gtg tac tat tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc 336
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 100 105 110
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 35 40 45
 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
 50 55 60

11

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
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<223> Oligonucleotide R5349

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gtacactgcg gtgtcctc 78

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tgtgaagacg t

71

<210> 79
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer P7997

<400> 79
ggaggtatgc tggtgacttg gatgtgtcta gagagaacgt gaatctgccc ttgaa 55

<210> 80
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer P7998

<400> 80
ccaagtcaac agcatacctc caaatgaata gcctgagagc agaggacacc gcagtgtact 60

at 62

<210> 81
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer P7993

<400> 81
gaattcggta ccctggcccc agtagtccat ggcataagat ctgtatcctc tagcacaata 60

gtacactgcg gtgtcctc 78

<210> 82
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer P7996

<400> 82
gaattcgtgc actctgaggt tcagctggtc 30

<210> 83
<211> 74

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5' Primer

 <400> 83
 cgcgcggaac ttgcagtggc cttggctggg ttcgctaccg tagcgcaagc tgacattcaa 60

 atgacccaga gccc 74

<210> 84
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' Primer

 <400> 84
 ttcaactgct catcagatgg 20

<210> 85
 <211> 78
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5' Primer

 <400> 85
 gctatcgcaa ttgcagtggc gctagctggg ttcgccaccg tggcgcaagc tgaggttcag 60

 ctggtcgagt caggaggc 78

<210> 86
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' Primer

 <400> 86
 gcctgagttc cagcacac 18

<210> 87
 <211> 23
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Human Group 1 consensus framework L1

<400> 87

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 88

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework L1

<400> 88

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys
20

<210> 89

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework L2

<400> 89

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 90

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework L2

<400> 90

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile Tyr
1 5 10 15

<210> 91
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework L3

<400> 91

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 92
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework L3

<400> 92

Gly Val Pro Tyr Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Thr Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys
20 25 30

<210> 93
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework L4

<400> 93

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1 5 10

<210> 94
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework L4

9

<400> 94

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
1 5 10

<210> 95

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework H1

<400> 95

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 96

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework H1

<400> 96

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr
20 25 30

<210> 97

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework H2

<400> 97

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 98
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework H2

<400> 98

Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met Gly
1 5 10

<210> 99
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework H3

<400> 99

Arg Val Thr Ile Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 100
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework H3

<400> 100

Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe Leu Gln
1 5 10 15

Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg
20 25 30

<210> 101
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 1 consensus framework H4

<400> 101

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 102

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework H4

<400> 102

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 103

<211> 324

<212> DNA

<213> Murine

<220>

<221> CDS

<222> (1)..(324)

<223>

<400> 103

gac att gtg atg acc cag tct caa aaa ttc atg tcc aca tca gta gga 48
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat 96
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

gta gcc tgg tat caa cag aaa cca gga caa tct cct aaa gca ctg att 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

tac tcg gca tcc ttc cta tat agt gga gtc cct tat cgc ttc aca ggc 192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly
50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc act gtg cag tct 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser
65 70 75 80

gaa gac ttg gca gag tat ttc tgt cag caa tat aac atc tat cct ctc 288
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
85 90 95

acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgt
 Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 100 105

324

<210> 104
 <211> 108
 <212> PRT
 <213> Murine

<400> 104

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
 1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30

C1

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser
 65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
 85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 100 105

<210> 105
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hTNF40 heavy chain variable domain

<220>
 <221> CDS
 <222> (1)..(354)
 <223>

<400> 105
 cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu

48

C

1	5	10	15	
aca gtc aag atc tcc tgc aag gct tct gga tat gtt ttc aca gac tat				96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr	20	25	30	
gga atg aat tgg gtg aag cag gct cca gga aag gct ttc aag tgg atg				144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met	35	40	45	
ggc tgg ata aac acc tac att gga gag cca ata tat gtt gat gac ttc				192
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe	50	55	60	
aag gga cga ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt				240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe	65	70	75	80
ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt				288
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys	85	90	95	
gca aga ggt tac cgg tcc tat gct atg gac tac tgg ggt caa gga acc				336
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr	100	105	110	
tca gtc acc gtc tct tca				354
Ser Val Thr Val Ser Ser	115			

<210> 106
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hTNF40 heavy chain variable domain

<400> 106

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu			
1	5	10	15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr	20	25	30
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met	35	40	45
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe	50	55	60

9

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 107
<211> 84
<212> DNA
<213> Artificial Sequence

C1
<220>
<223> OmpA oligonucleotide adaptor

<220>
<221> CDS
<222> (29) .. (67)
<223>

<400> 107
tcgagttcta gataacgagg cgtaaaaa atg aaa aag aca gct atc gca att 52
Met Lys Lys Thr Ala Ile Ala Ile
1 5

gca gtg gcc ttg gct ctgacgtacg agtcagg 84
Ala Val Ala Leu Ala
10

<210> 108
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> OmpA oligonucleotide adaptor

<400> 108

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala
1 5 10

<210> 109
<211> 67
<212> DNA

2

<213> Artificial Sequence

<220>

<223> IGS cassette-1

<220>

<221> CDS

<222> (2) .. (40)

<223>

<220>

<221> CDS

<222> (43) .. (66)

<223>

<400> 109

g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt ta atg aag 48
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Met Lys
1 5 10 15

C1 aag act gct ata gca att g 67
Lys Thr Ala Ile Ala Ile
20

<210> 110

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> IGS cassette-1

<400> 110

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

<210> 111

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> IGS cassette-1

<400> 111

Met Lys Lys Thr Ala Ile Ala Ile
1 5

<210> 112

<211> 69

C

<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-2

<220>
<221> CDS
<222> (2)..(43)
<223>

<220>
<221> CDS
<222> (45)..(68)
<223>

C1
<400> 112
g agc tca cca gta aca aaa agt ttt aat aga ggg gag tgt taa a atg 47
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Met
1 5 10

aag aag act gct ata gca att g 69
Lys Lys Thr Ala Ile Ala Ile
15 20

<210> 113
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-2

<400> 113
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

<210> 114
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-2

<400> 114
Met Lys Lys Thr Ala Ile Ala Ile
1 5

<210> 115

C

<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-3

<220>
<221> CDS
<222> (2)..(43)
<223>

<220>
<221> CDS
<222> (57)..(80)
<223>

<400> 115
g agc tca cca gta aca aaa agc ttt aat aga gga gag tgt tga 43
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

CI
ggaggaaaaa aaa atg aag aaa act gct ata gca att g 81
Met Lys Lys Thr Ala Ile Ala Ile
15 20

<210> 116
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-3

<400> 116

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

<210> 117
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-3

<400> 117

Met Lys Lys Thr Ala Ile Ala Ile
1 5

C

<210> 118
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> IGS cassette-4

<220>
<221> CDS
<222> (2)..(43)
<223>

<220>
<221> CDS
<222> (57)..(80)
<223>

<400> 118
g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt tga 43
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

cgaggattat ata atg aag aaa act gct ata gca att g 81
Met Lys Lys Thr Ala Ile Ala Ile
15 20

<210> 119
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-4

<400> 119

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1 5 10

<210> 120
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> IGS cassette-4

<400> 120

Met Lys Lys Thr Ala Ile Ala Ile
1 5

<210> 121
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 3 consensus framework H1

<400> 121

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

<210> 122
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 3 consensus framework H2

<400> 122

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 123
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Human group 3 consensus framework H3

<400> 123

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 124
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Human group 3 consensus framework H4

<400> 124

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 125

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for fab

<400> 125

gagggttcagc tggtcgagtc aggaggcggc ctcgtgcagc ctggcggatc actgagattg 60
tcctgtgctg catctgggta cgtcttcaca gactatggaa tgaattgggt tagacaggcc 120
ccgggaaagg gcctggaatg gatggggttg attaatactt acattggaga gcctatttat 180
C) gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240
ctccaaatga atagcctgag agcagaggac accgcagtggt actattgtgc tagaggatac 300
agatcttatg ccatggacta ctggggccag ggtaccctag tcacagtctc ctcagcttcc 360
accaagggcc catcgggtctt ccccttgcca cctcctcca agagcacctc tgggggcaca 420
gcggccctgg gctgcctggc caaggactac ttccccgaac cggtgacggg gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggctcgaca agaaagtt 648

<210> 126

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for fab

<400> 126

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr
20 25 30

α

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val
210 215

<210> 127

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted light chain for fab and modified fab

<400> 127
 gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60
 atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca gcaaaaacca 120
 ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180
 aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca 240
 gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcgggtcag 300
 ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taactttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

C1
 <210> 128
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Grafted light chain for fab and modified fab

<400> 128

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
 85 90 95

C

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 129
<211> 687
<212> DNA
<213> Artificial Sequence

<220>
<223> Grafted heavy chain for modified fab

<400> 129
gaggttcagc tggtcgagtc aggaggcggc ctcgtgcagc ctggcggatc actgagattg 60
tcctgtgctg catctgggta cgtcttcaca gactatggaa tgaattgggt tagacaggcc 120
ccgggaaagg gcctggaatg gatggggttgg attaatactt acattggaga gcctatztat 180
gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240
ctccaaatga atagcctgag agcagaggac accgcagtgt actattgtgc tagaggatac 300
agatcttatg ccatggacta ctggggccag ggtaccctag tcacagtctc ctcagcttcc 360
accaagggcc catcggtctt ccccttgga cctcctcca agagcacctc tgggggcaca 420
gcggccctgg gctgcctggc caaggactac ttccccgaac cggtgacggc gtcgtggaac 480

145

150

155

160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

C1 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Ala Ala
225

C